

#4

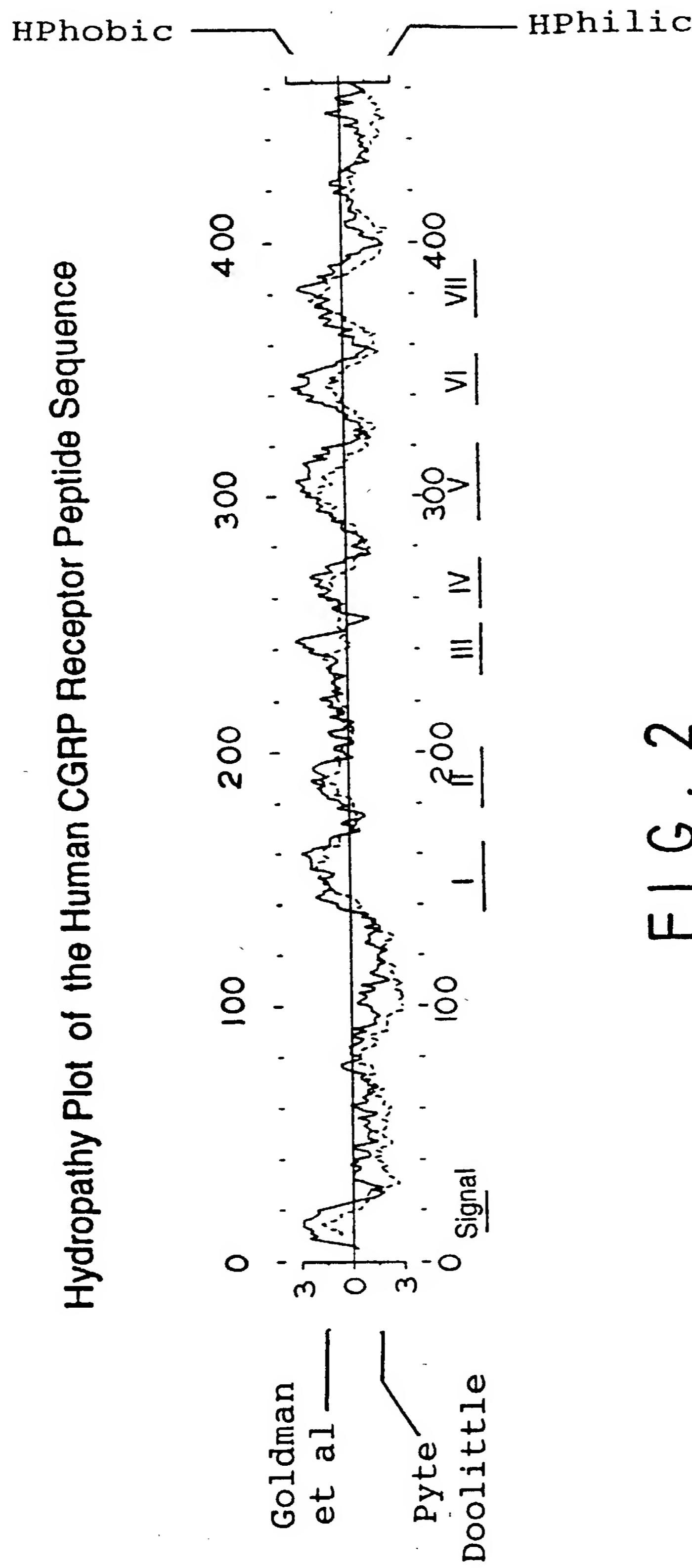
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atg gag aaa aag tgt acc ctg tat ttt ctg gtt ctc ttg cct ttt ttt atg att ctt gtt  
1 M E K K C T L Y F L V L L P F F M I L V 60  
aca gca gaa tta gaa gag agt cct gag gac tca att cag ttg gga gtt act aga aat aaa  
21 T A E L E S P E D S I Q L G V T R N K 120  
atc atg aca gctcaa tat gaa tgt tac caa aag att atg caa gac ccc att caa caa gca  
41 I M T A Q Y E C Y Q K I M Q D P I Q Q A 180  
gaa ggc gtt tac tgc aac aga acc tgg gat gga tgg ctc tgc tgg aac gat gtt gca gca  
61 E G V Y C N R T W D G W L C W N D V A A 240  
gga act gaa tca atg cag ctc tgc cct gat tac ttt cag gac ttt gat cca tca gaa aaa  
81 G T E S M Q L C P D Y F Q D F D P S E K 300  
gtt aca aag atc tgt gac caa gat gga aac tgg ttt aga cat cca gca agc aac aga aca  
101 V T K I C D Q D G N W F R H P A S N R T 360  
tgg aca aat tat acc cag tgt aat gtt aac acc cac gag aaa gtg aag act gca cta aat  
121 W T N Y T Q C N V N T H E K V K T A L N 420  
ttg ttt tac ctg acc ata att gga cac gga ttg tct att gca tca ctg ctt atc tcg ctt  
141 L F Y L T I I G H G L S I A S L L I S L 480  
ggc ata ttc ttt tat ttc aag agc cta agt tgc caa agg att acc tta cac aaa aat ctg  
161 G I F F Y F K S L S C Q R I T L H K N L 540  
ttc ttc tca ttt gtt tgt aac tct gtt gta aca atc att cac ctc act gca gtg gcc aac  
181 F F S F V C N S V V T I I H L T A V A N 600  
aac cag gcc tta gta gcc aca aat cct gtt agt tgc aaa gtg tcc cag ttc att cat ctt  
201 N Q A L V A T N P V S C K V S Q F I H L 660  
tac ctg atg ggc tgt aat tac ttt tgg atg ctc tgt gaa ggc att tac cta cac aca ctc  
221 Y L M G C N Y F W M L C E G I Y L H T L 720  
att gtg gtg gcc gtg ttt gca gag aag caa cat tta atg tgg tat tat ttt ctt ggc tgg  
241 I V V A V F A E K Q H L M W Y Y F L G W 780  
gga ttt cca ctg att cct gct tgt ata cat gcc att gct aga agc tta tat tac aat gac  
261 G F P L I P A C I H A I A R S L Y Y N D 840  
aat tgc tgg atc agt tct gat acc cat ctc ctc tac att atc cat ggc cca att tgt gct  
281 N C W I S S D T H L L Y I I H G P I C A 900  
gct tta ctg gtg aat ctt ttt ttc ttg tta aat att gta cgc gtt ctc atc acc aag tta  
300 A L L V N L F F L L N I V R V L I T K L 960  
aaa gtt aca cac caa gcg gaa tcc aat ctg tac atg aaa gct gtg aga gct act ctt atc  
321 K V T H O A E S N L Y M K A V R A T L I 1020

FIG. 1A

ttg gtg cca ttg ctt ggc att gaa ttt gtg ctg att cca tgg cga cct gaa gga aag att  
341 L V P L L G I E F V L I P W R P E G K I 1080  
gca gag gag gta tat gac tac atc atg cac atc ctt atg cac ttc cag ggt ctt ttg gtc  
381 A E E V Y D Y I M H I L M H F Q G L L V 1140  
tct acc att ttc tgc ttc ttt aat gga gag gtt caa gca att ctg aga aga aac tgg aat  
401 S T I F C F N G E V Q A I L R R N W N 1200  
caa tac aaa atc caa ttt gga aac agc ttt tcc aac tca gaa gct ctt cgt agt gcg tct  
421 Q Y K I Q F G N S F S N S E A L R S A S 1260  
tac aca gtg tca aca atc agt gat ggt cca ggt tat agt cat gac tgt cct agt gaa cac  
441 Y T V S T I S D G P G Y S H D C P S E H 1320  
tta aat gga aaa agc atc cat gat att gaa aat gtt ctc tta aaa cca gaa aat tta tat  
462 L N G K S I H D I E N V L L K P E N L Y 1380  
aat tga aaatagaaggatgggtgtctcaactgtttgggtgcttctcctaactcaaggactggaccatgactctgttag  
N  
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aatcaatgaaggattcttattttcttggatttgtaaaaagaaattgtgaaaaatgagcttgcataactccattat 2326  
tttattttatgtctcaatcaaatacataacctatgtattttaagcaaatataatgcaacaatgtgttat 2405  
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FIG. 1B



E I G H T

FIG. 3

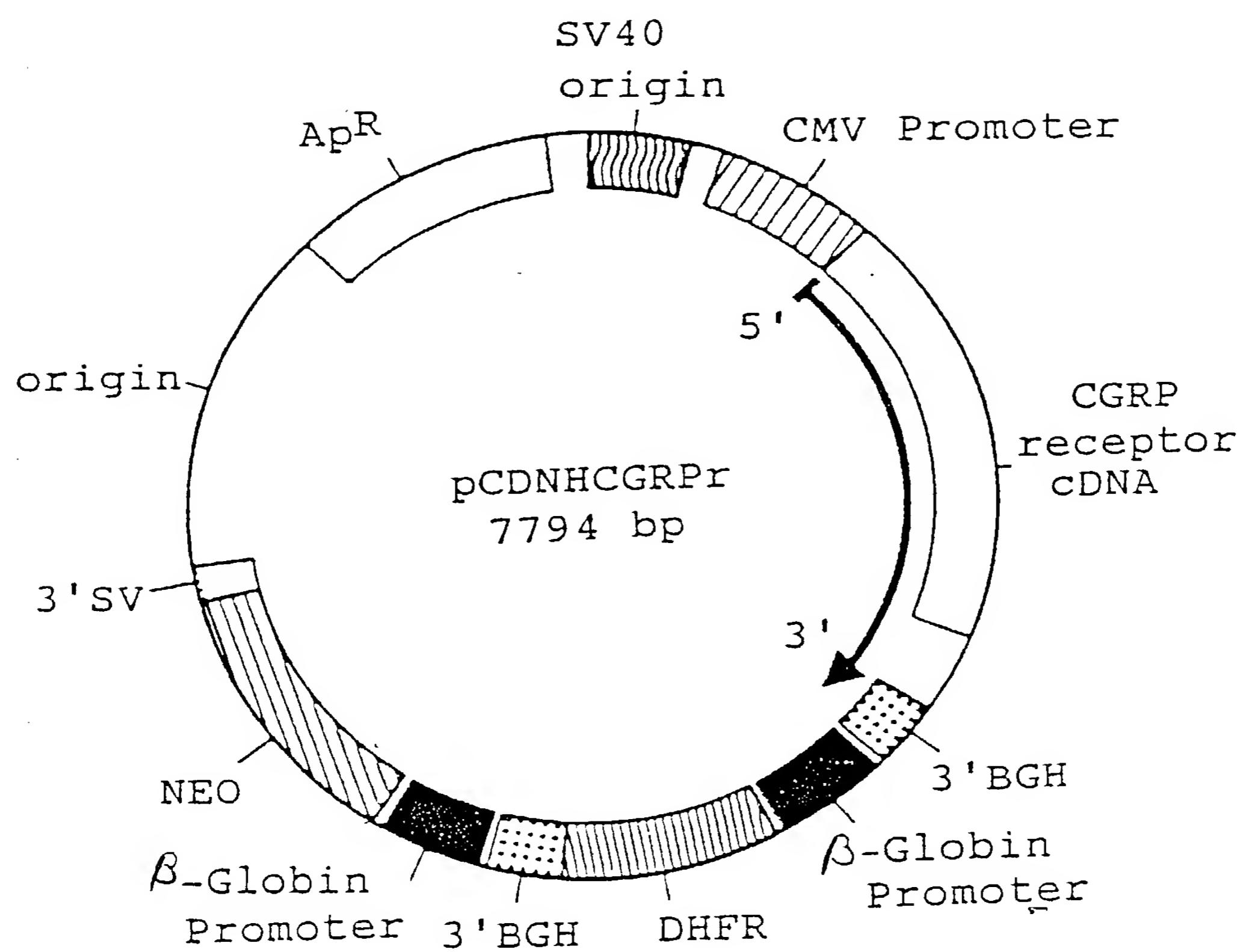
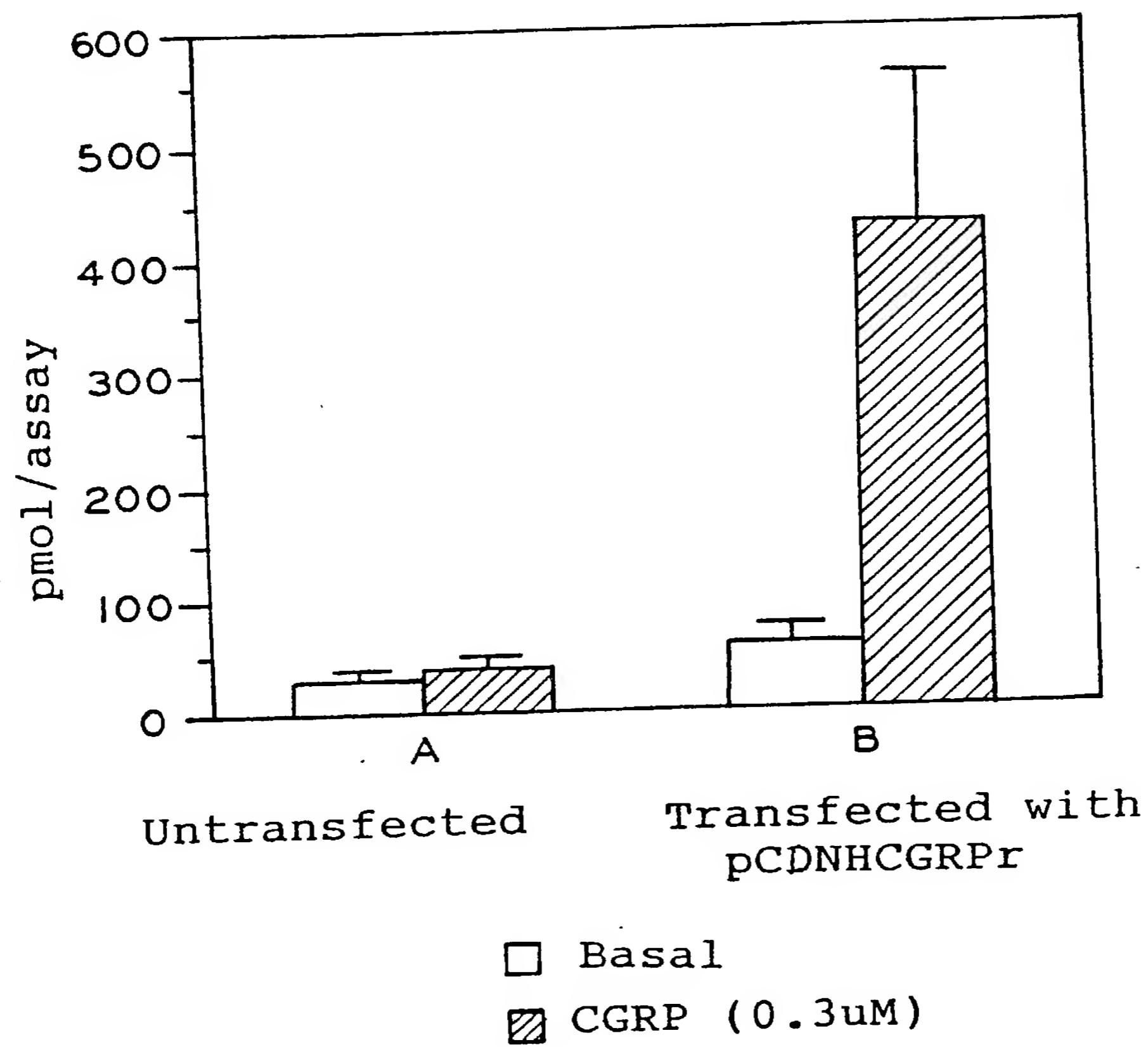


FIG. 4

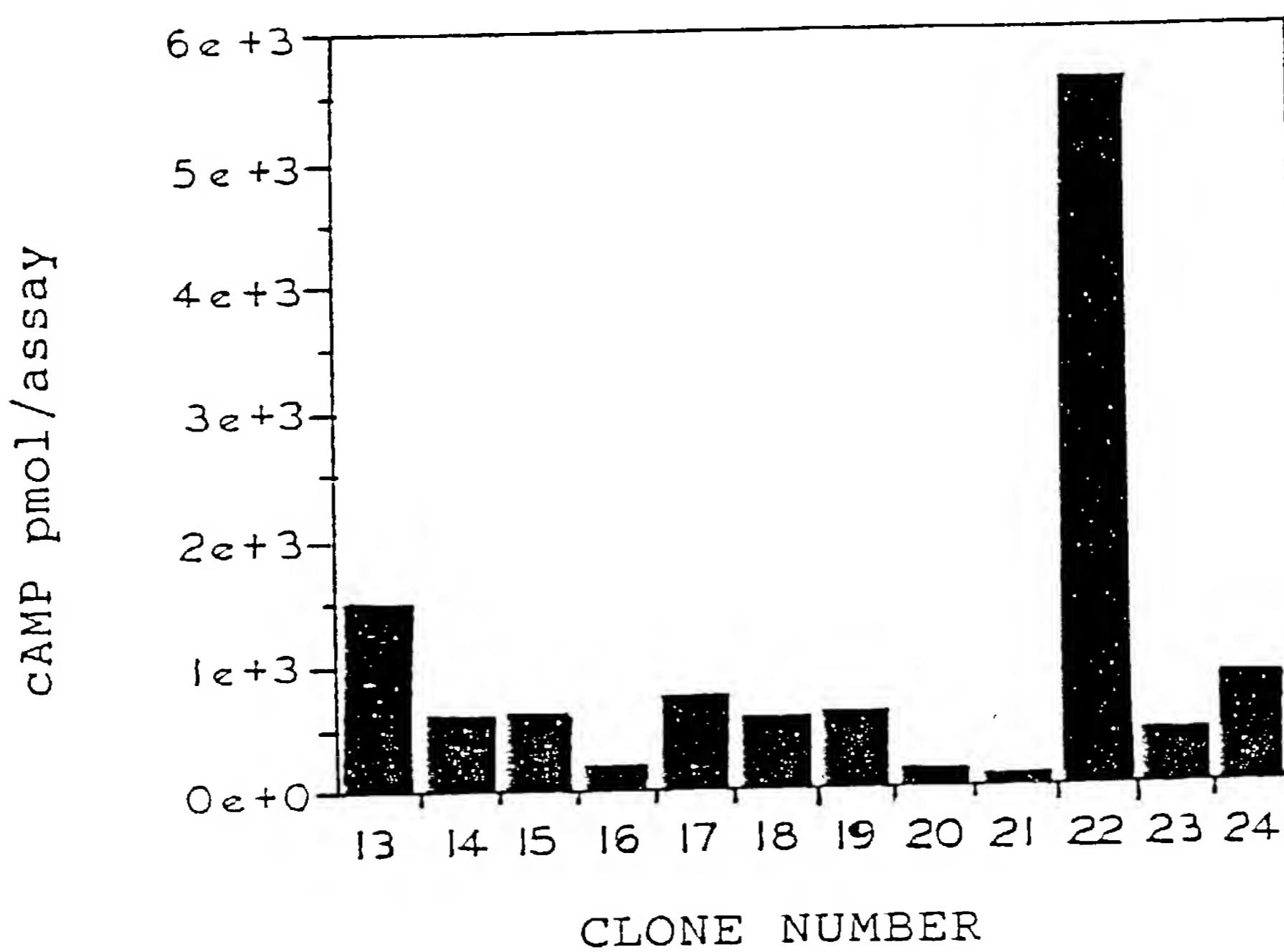
cAMP RESPONSE IN 293 CELLS



2. 23 23 23 23 23 23 23 23 23 23

F I G. 5

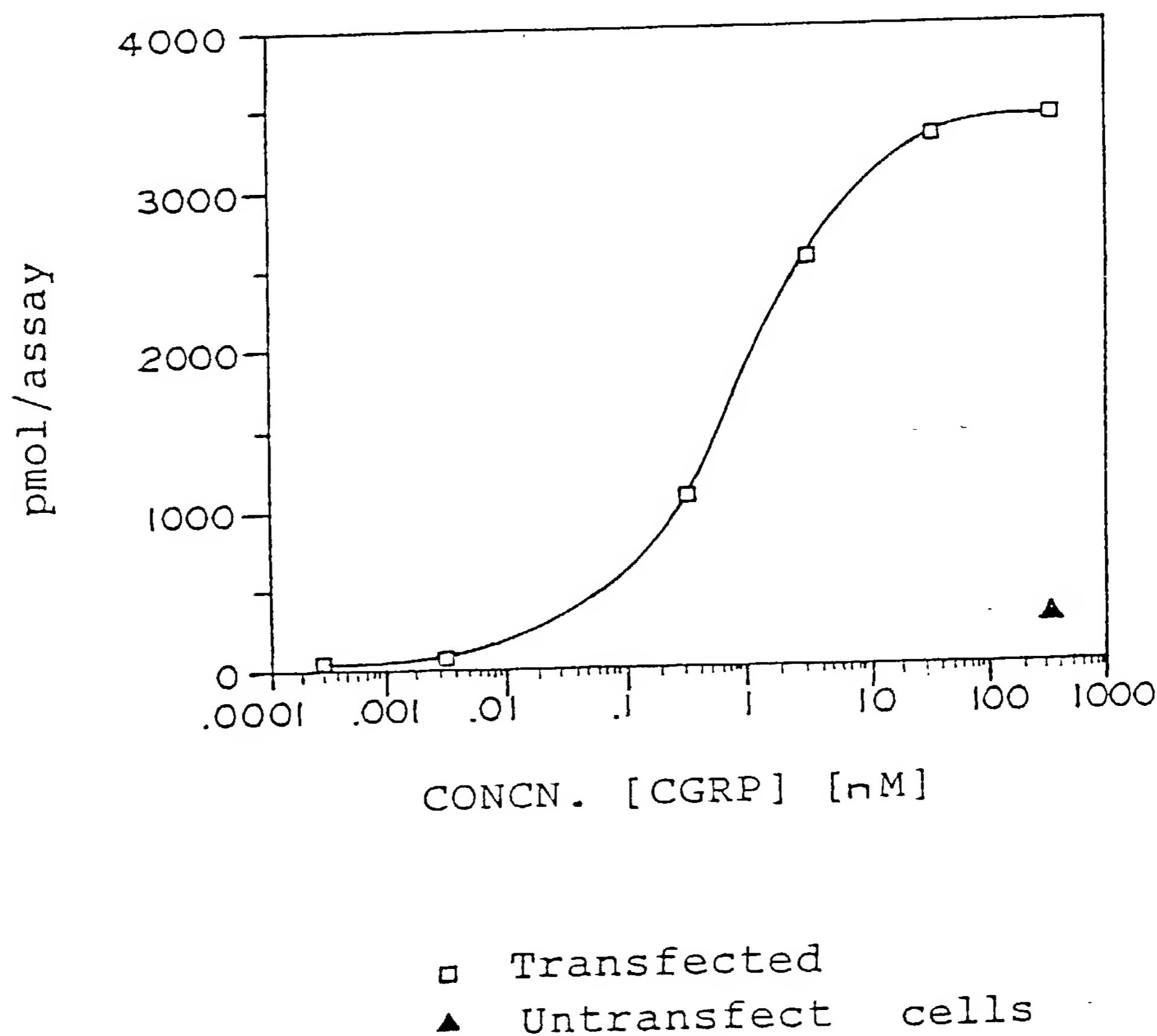
EFFECT OF CGRP TREATMENT OF 293  
CELL LINES STABLY TRANSFORMED  
WITH THE pCDNHCGRPr CONSTRUCT



3.03 0.5 3.03 0.5 3.03 0.5 3.03 0.5

F I G. 6

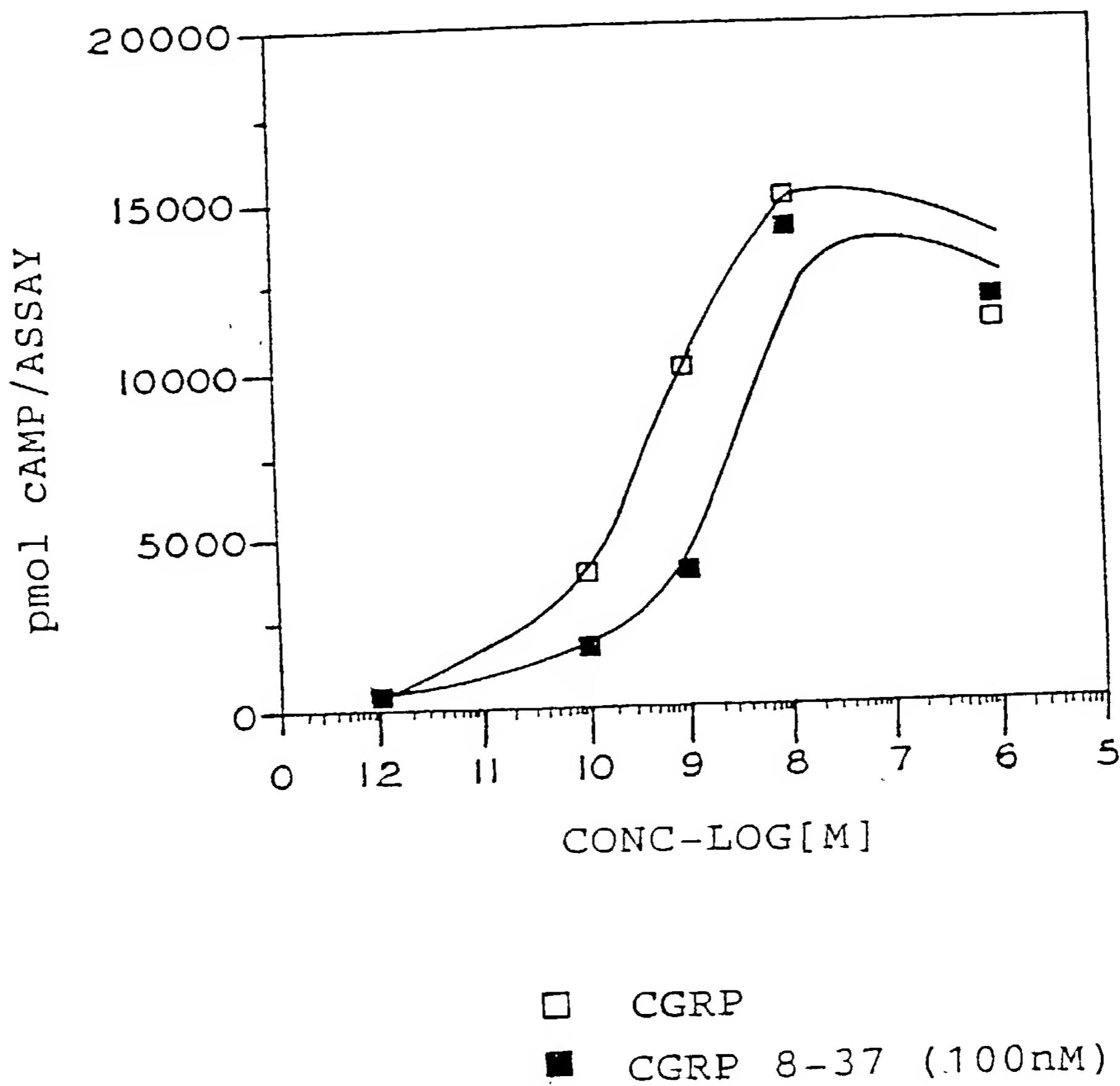
CGRP-MEDIATED cAMP IN pCDNHCRPr STABLY  
TRANSFORMED 293 CELLS (CLONE 22)



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FIG. 7

EFFECT OF CGRP8-37 ON CGRP-MEDIATED  
cAMP IN pCDNHCGRPr STABLY  
TRANSFORMED 293 CELLS (CLONE 22)



[125I]CGRP BINDING TO PCDNHCGPr TRANSFORMED  
293 CELLS (CLONE 22) MEMBRANES

FIG. 8 A

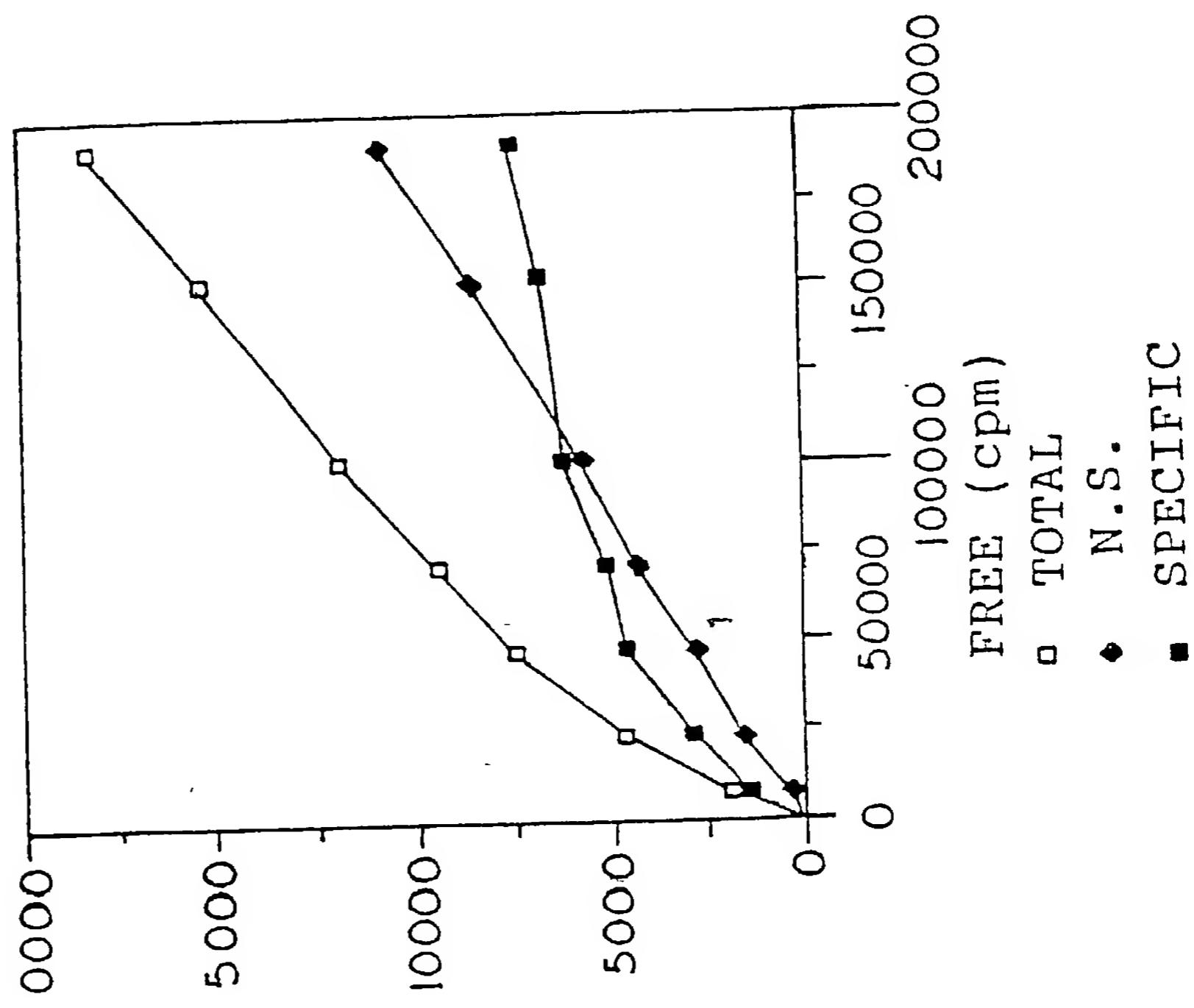


FIG. 8 B

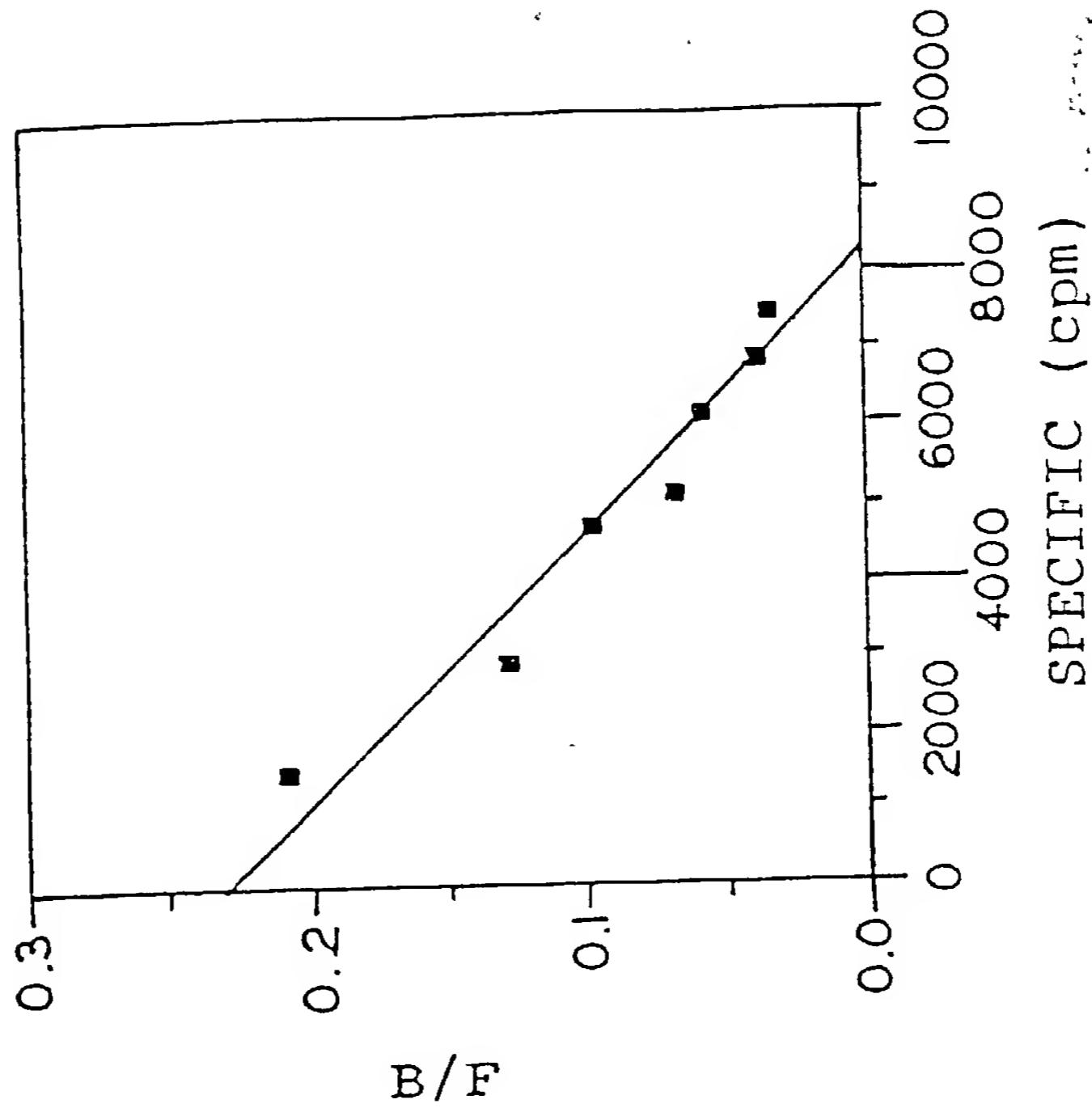
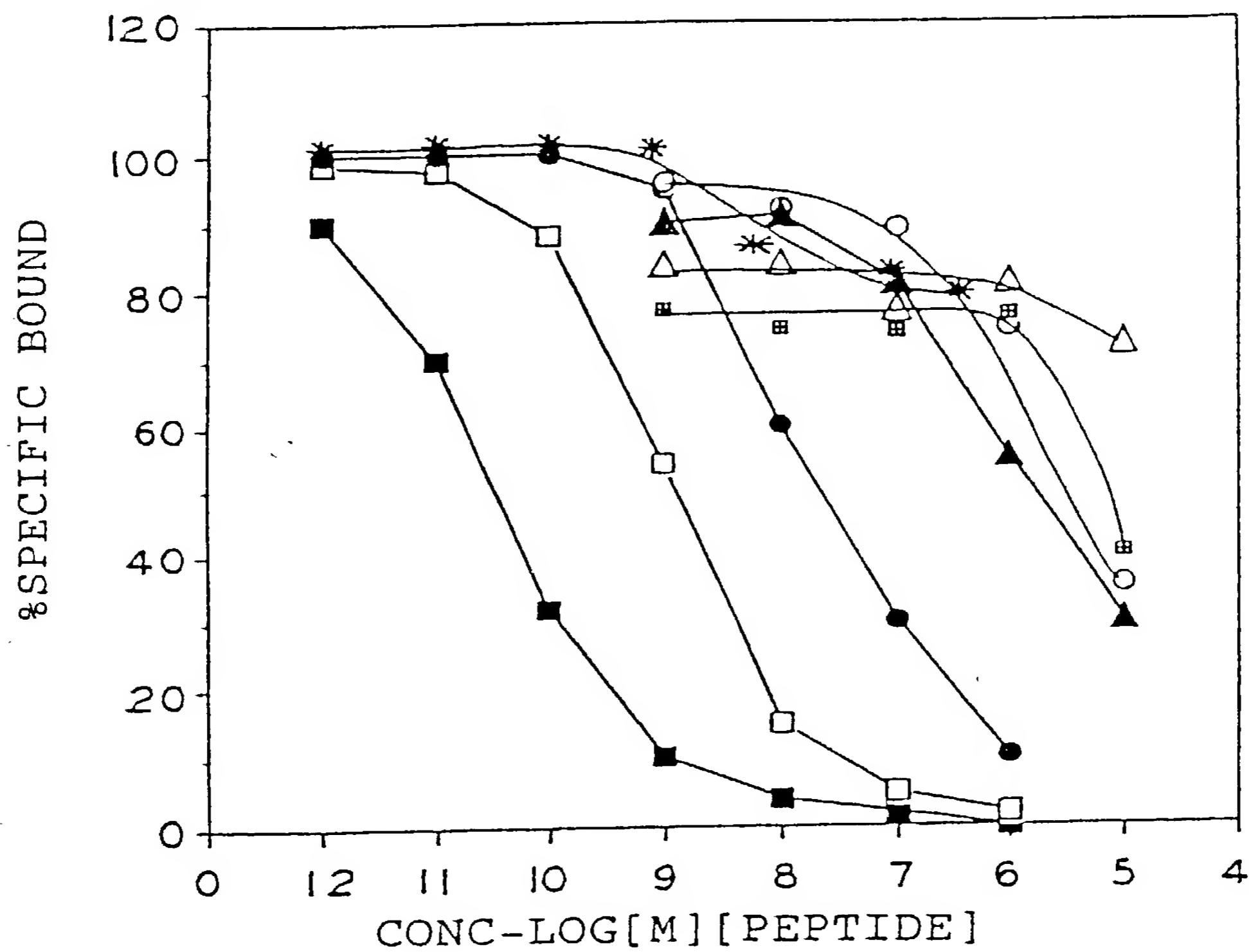


FIG. 9

COMPETITION CURVES FOR  
REPRESENTATIVE CGRP ANALOGS AGAINST  
[125I]CGRP BINDING IN pCDNHCGRPr  
TRANSFORMED CELL (CLONE22) MEMBRANES



CGRP > CGRP8-37 > ADM > SCT8-32 > SCT > VIP > Amylin, LCT

Diagram showing six lines with markers: a black square, an open square, a black circle, an open circle, a black triangle, and an open triangle.

# Comparison of Human CGRP and Human Calcitonin Receptor Amino Acid Sequences

## MATCH WITH FIG. 10A

## F | G | O B

|     |   |     |  |
|-----|---|-----|--|
| 201 | KNMFLTYILNSMIIHLVEVVPNGELVRRDPVSCKILHFFHQYMMACNY      | 250 |  |
| 228 | FWMLCEGIVYLHTLIVVAVFAEKQHLMWYYFLGWGFPPLIPACIHAIARSLY  | 277 |  |
| 251 | FWMLCEGIVYLHTLIVVAVFTEKQRLRWYYLLGWGFPPLVPTTIHAITRAVY  | 300 |  |
| 278 | YNDNCWISSDTHLLYIITHGPICAALLVNLIFFLLNIVRVVLITKLKVTHQAE | 327 |  |
| 301 | FNDNCWLSVETHLLYIITHGPVMAALVVNEFFFLNIVRVVLVTKMRETHEAE  | 350 |  |
| 328 | SNLYMKAVRATLILVPLLGIEFVLIIPWRPEGKIAEEVYDYIMHTLMHFQG   | 377 |  |
| 351 | SHMYLKAVKATMILVPLLGIQFVVFWRPSNPKMLGKIYDYVMHSLIHFQG    | 400 |  |
| 378 | LLVSTIFCFNGEVQAILRRNNQYKIQFGNSFSNSEALRSASYTYSTIS      | 427 |  |
| 401 | FFVATIYCFCNNEVQTTVKRQWAQFKIQWNQRWGRPSNRSARAIAAE       | 450 |  |
| 428 | DGPGYSHDCPSEHLNGKS. IHDIENVLLKPENLYN.....             | 461 |  |
| 451 | AGDIPPIYICHQEPRNEPANNQGEESAEIIPNIEQESSA               | 490 |  |

**F I G. II A**  
**Comparison of Human**  
**and Rat CGRP Receptor Amino Acid Sequences**

|   |  |            |
|---|--|------------|
| 1   | MEKKCTLYFLVLLPFFMILVTAEEESPEDSISIQLGVTRNKIMTAQYECY   | 49         |
| 1   | :    :  .   :   :   :   :   :   :   :   :   :   :    |            |
| 1   | MMDKKCTLCFLFLLLNMALIAAESEEGANQT. DLGVTRNKIMTAQYECY   | 49         |
| 50  | OKIMQDPIQQAEGVYCNRTWDGWLWNDVAAGTESMQLCPDYFQDFDPSE    | 99         |
| :    :   :    :    :    :    :    :    :    :    :  |  |            |
| 50  | OKIMQDPIQQGEGLYCNRTWDGWLWNDVAAGTESMQICPDYFQDFDPSE    | 99         |
| 100   | KVTKKICDQDGNNWFRHPASNRWTNTYQCNVNNTHEKVKTALNLFYLTIGH  | 149        |
| :    :    :    :    :    :    :    :    :    :    : |  |            |
| 100   | KVTKKICDQDGNNWFRHPDSNRTWTNTYTLCNNSTHEKEKTALNLFYLTIGH | 149        |
| 150   | GLSIASLILSICIFFYFKSLSQQRITLHKNLFFSFVCNSVVTIIHLTAVA   | 199        |
| :    :    :    :    :    :    :    :    :    :    : |  |            |
| 150   | GLSIASLILSIIIFFYFKSLSQQRITLHKNLFFSFVCNSIVTIIHLTAVA   | 199        |
| 150   | <u>   </u>   | <u>   </u> |
| 200   | NNQALVATNPVSCKVSQFIHLYLMGCNYFWMCLCEGIYLHTLIVVAVFAEK  | 249        |
| :    :    :    :    :    :    :    :    :    :      |  |            |
| 200   | NNQALVATNPVSCKVSQFIHLYLMGCNYFWMCLCEGIYLHTLIVVAVFAEK  | 249        |
| 200   | <u>   </u>   | <u>   </u> |

**MATCH WITH FIG. II B**

MATCH WITH FIG. 11A

F | G . || B

250 QHLMWYYFLGWFPLIPACIHAIARSLYYNDNCWISSDTHLLYIITHGPIC 299  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
250 QHLMWYYFLGWFPLIPACIHAIARSLYYNDNCWISSDTHLLYIITHGPIC 299  
—V— .  
300 AALLVNLFFLNNIVRVVLITKLKVTHQAESNLYMKAVRATLILVPLLGIEF 349  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
300 AALLVNLFFLNNIVRVVLITKLKVTHQAESNLYMKAVRATLILVPLLGIEF 349  
—V— .  
350 VLIPWRPEGKIAEEVYDYIMHILMHFQGLLVSTIFCFFNGEVQAILRRNW 399  
||:|||||:|||||:|||||:|||||:  
350 VLFPWRPEGKVAEEVYDYVMHILMHYQGLLVSTIFCFFNGEVQAILRRNW 399  
—V— .  
400 NQYKIQFGNSFSNSEALRSASYTVSTISDGPGYSHDCPSEHLNNGKSIHDI 449  
||:|||||:||:|||||:|||||:  
400 NQYKIQFGNGFISHSDALRSASYTVSTISDVQGYSHDCPTEHLNNGKSIQDI 449  
—VII— .  
450 ENVLLKPNLYN... 461  
||:|||||:  
450 ENVALKPEKMYDLVM 464